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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/090,378

DATE: 05/01/2002

TIME: 11:53:16

Input Set : N:\Crf3\RULE60\10090378.raw

Output Set: N:\CRF3\05012002\J090378.raw

1 <110> APPLICANT: Panganiban, Antonito
 2 Callahan, Mark A.
 3 <120> TITLE OF INVENTION: Method of Identifying Modulators of HIV-1 VPU and GAG
 4 Interaction with U Binding Protein (UBP)
 5 <130> FILE REFERENCE: 960296.95335
 6 <140> CURRENT APPLICATION NUMBER: 10/090,378
 7 <141> CURRENT FILING DATE: 2002-03-04
 9 <150> PRIOR APPLICATION NUMBER: US/09/301,978C
 10 <151> PRIOR FILING DATE: 1999-04-29
 13 <150> PRIOR APPLICATION NUMBER: 60/083,567
 14 <151> PRIOR FILING DATE: 1998-04-30
 15 <160> NUMBER OF SEQ ID NOS: 29
 16 <170> SOFTWARE: PatentIn Ver. 2.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 2221
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Homo sapiens
 22 <220> FEATURE:
 23 <221> NAME/KEY: unsure
 24 <222> LOCATION: (1514)
 25 <223> OTHER INFORMATION: n = any nucleotide.
 26 <221> NAME/KEY: unsure
 27 <222> LOCATION: (2066)
 28 <223> OTHER INFORMATION: n = any nucleotide.

ENTERED

W--> 29 <400> 1

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30   tcggtcgctt gagaggtatc acctcttctg ggctcaagat ggacaacaag aagcgcctgg 60
31   cctacgccat catccagttc ctgcatgacc agctccggca cgggggcctc tcgtccgatg 120
32   ctccaggagc cttggaagtc gccatccagt gcctggagac tgcgtttggg gtgacggtag 180
33   aagacagtga ccttgcgctc cctcagactc tgccggagat atttgaagcg gctgccacgg 240
34   gcaaggagat gccgcaggac ctgaggagcc cagcgcgaac cccgccttcc gaggaggact 300
35   cagcagaggc agagcgcctc aaaaccgaag gaaacgagca gatgaaagtg gaaaactttg 360
36   aagctgccgt gcatttctac ggaaaagcca tcgagctcaa cccagccaac gccgtctatt 420
37   tctgcaacag agccgcagcc tacagcaaac tcggcaacta cgcaggcgcg gtgcaggact 480
38   gtgagcgggc catctgcatt gacccggcct acagcaaggc ctacggcagg atgggccttg 540
39   cgctctccag cctcaacaag cacgtggagg ccgtggctta ctacaagaag gcgctggagc 600
40   tggacccga caacgagaca tacaagtcca acctcaagat agcggagctg aagctgcggg 660
41   agggcccccag cccacggga ggcgtgggca gcttcgacat cgcggcctg ctgaacaacc 720
42   ctggcttcag gagcatggct tcgaacctaa tgaacaatcc ccagattcag cagctcatgt 780
43   ccggcatgat ttcgggtggc aacaaccctt tgggaactcc cggcaccagc ccctgcgaga 840
44   acgacctggc cagcctcatc caggcggggc agcagtttgc ccagcagatg cagcagcaga 900
45   acccagagtt gatagagcag ctccaggagc aatccggagt cggacgcca gcgccagcaa 960
46   cgacgaccag caggagtgc gctgcctgct cccgggtgtga ccgctcctt ccctggccga 1020
47   cccgaaggaa gccttctggt tgtctgccac ttcctcctgt tggactgcct gagagagggg 1080

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48 aagagagaga cctcggacct gcatgtcaag atggattttc ccctttttatc tctgccctcc 1140
49 tccactccct ttttgtaact cccttacagc ccccagaccc ttcttgaaac gagagccagc 1200
50 aagctgagca cagaccagca ggcacctccc ttccagcccc cagaaagctc ggtcacttga 1260
51 gtgtttttcta gaatcctggg gtgtctcccg ggcgtctca gagaagtggc aggtttcacg 1320
52 ttcagccgtg tggcggatcg tgtggtttcc aaagcctttt acagcccccg ccccccattc 1380
53 cgtggtctgt ctgcaggaaac tctcccgctc gtgagaagcc tctttccgag tgcacctccc 1440
54 ggccaccccg gccctgtgcc tgctcggaag agctcactgc cagctgcggc ctgggcaccg 1500
W--> 55 cgggccatgt gtgnttgcac gaggaactct ttagtggcag acacctaaaga gacggctgcg 1560
56 gtcaccccac gccctccgtg ctcaggagcc gtccctgggtg cataggacca gtttctgtga 1620
57 cttttctcca gtggggcatg ttgacagaca tgtttccct cctccacccc tcattttctg 1680
58 gtccctcgca ctgagagcca ggggcgacat catgaccttc tgtcccgccc gccttagccc 1740
59 cgggaacagg gaaggagct gggccgtttc tgtctgtgtc ccatcctgct gtccttctgt 1800
60 cctgatggt tcatggccc ggggcccccc agggaagctt acccctcctg tgcctgggtg 1860
61 aggccacggg acacctcagg tgccaccac cttggcccta aaacagccac caggaaagca 1920
62 gccgagagc cggacagcgg gcagcctgtc tgggttctg aggcctgggg gtggcagacg 1980
63 aaccacggc gccgtggtc cagcagcagg gttgtcagtc ggagcatcct ggggctccct 2040
W--> 64 ggctcctggc cgtctgtgag gtaggngcag taccgtgtat cgtaggtagc agtaggaacg 2100
65 ggggccaccg cggccctgca gccgttcagc gcggtgaggt gtgtgccaag cccaccggg 2160
66 gtgcagggcg tgacgtgtgg ggaataaata ggcgttgtga cctcaaaaaa aaaaaaaaaa 2220
67 a 2221
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70 <211> LENGTH: 382
71 <212> TYPE: PRT
72 <213> ORGANISM: Homo sapiens
73 <400> SEQUENCE: 2
74 Met Asp Asn Lys Lys Arg Leu Ala Tyr Ala Ile Ile Gln Phe Leu His
75 1 5 10 15
76 Asp Gln Leu Arg His Gly Gly Leu Ser Ser Asp Ala Gln Glu Ser Leu
77 20 25 30
78 Glu Val Ala Ile Gln Cys Leu Glu Thr Ala Phe Gly Val Thr Val Glu
79 35 40 45
80 Asp Ser Asp Leu Ala Leu Pro Gln Thr Leu Pro Glu Ile Phe Glu Ala
81 50 55 60
82 Ala Ala Thr Gly Lys Glu Met Pro Gln Asp Leu Arg Ser Pro Ala Arg
83 65 70 75 80
84 Thr Pro Pro Ser Glu Glu Asp Ser Ala Glu Ala Glu Arg Leu Lys Thr
85 85 90 95
86 Glu Gly Asn Glu Gln Met Lys Val Glu Asn Phe Glu Ala Ala Val His
87 100 105 110
88 Phe Tyr Gly Lys Ala Ile Glu Leu Asn Pro Ala Asn Ala Val Tyr Phe
89 115 120 125
90 Cys Asn Arg Ala Ala Ala Tyr Ser Lys Leu Gly Asn Tyr Ala Gly Ala
91 130 135 140
92 Val Gln Asp Cys Glu Arg Ala Ile Cys Ile Asp Pro Ala Tyr Ser Lys
93 145 150 155 160
94 Ala Tyr Gly Arg Met Gly Leu Ala Leu Ser Ser Leu Asn Lys His Val
95 165 170 175
96 Glu Ala Val Ala Tyr Tyr Lys Lys Ala Leu Glu Leu Asp Pro Asp Asn
97 180 185 190

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Input Set : N:\Crif3\RULE60\10090378.raw

Output Set: N:\CRF3\05012002\J090378.raw

```

98      Glu Thr Tyr Lys Ser Asn Leu Lys Ile Ala Glu Leu Lys Leu Arg Glu
99          195                200                205
100     Ala Pro Ser Pro Thr Gly Gly Val Gly Ser Phe Asp Ile Ala Gly Leu
101          210                215                220
102     Leu Asn Asn Pro Gly Phe Met Ser Met Ala Ser Asn Leu Met Asn Asn
103          225                230                235                240
104     Pro Gln Ile Gln Gln Leu Met Ser Gly Met Ile Ser Gly Gly Asn Asn
105          245                250                255
106     Pro Leu Gly Thr Pro Gly Thr Ser Pro Ser Gln Asn Asp Leu Ala Ser
107          260                265                270
108     Leu Ile Gln Ala Gly Gln Gln Phe Ala Gln Gln Met Gln Gln Gln Asn
109          275                280                285
110     Pro Glu Leu Ile Glu Gln Leu Arg Ser Gln Ser Gly Val Gly Arg Pro
111          290                295                300
112     Ala Pro Ala Thr Thr Thr Ser Arg Ser Asp Ala Ala Cys Ser Arg Cys
113          305                310                315                320
114     Asp Arg Val Leu Pro Trp Pro Thr Arg Arg Lys Pro Ser Gly Cys Leu
115          325                330                335
116     Pro Leu Pro Pro Val Gly Leu Pro Glu Arg Gly Glu Glu Arg Asp Leu
117          340                345                350
118     Gly Pro Ala Cys Gln Asp Gly Phe Ser Pro Phe Ile Ser Ala Leu Leu
119          355                360                365
120     His Ser Leu Phe Val Thr Pro Leu Gln Pro Pro Asp Pro Ser
121          370                375                380
123 <210> SEQ ID NO: 3
124 <211> LENGTH: 23
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
129     Primer
130 <400> SEQUENCE: 3
131     agtagtacat catatgcaac cta                                     23
133 <210> SEQ ID NO: 4
134 <211> LENGTH: 21
135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial Sequence
137 <220> FEATURE:
138 <223> OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
139     Primer
140 <400> SEQUENCE: 4
141     tccacacagg atccccataa t                                       21
143 <210> SEQ ID NO: 5
144 <211> LENGTH: 31
145 <212> TYPE: DNA
146 <213> ORGANISM: Artificial Sequence
147 <220> FEATURE:
148 <223> OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
149     Primer

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Input Set : N:\Crf3\RULE60\10090378.raw

Output Set: N:\CRF3\05012002\J090378.raw

150 <400> SEQUENCE: 5
151 cgggatccgg tgcgagagcg tcggtattaa g 31
153 <210> SEQ ID NO: 6
154 <211> LENGTH: 28
155 <212> TYPE: DNA
156 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
159 Primer
160 <400> SEQUENCE: 6
161 gctctagacc tgtatctaata agagcttc 28
163 <210> SEQ ID NO: 7
164 <211> LENGTH: 21
165 <212> TYPE: DNA
166 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
169 Primer
170 <400> SEQUENCE: 7
171 ggccagatga gagaaccaag g 21
173 <210> SEQ ID NO: 8
174 <211> LENGTH: 27
175 <212> TYPE: DNA
176 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
179 Primer
180 <400> SEQUENCE: 8
181 caaagagtga cttaagggaa gctaaag 27
183 <210> SEQ ID NO: 9
184 <211> LENGTH: 21
185 <212> TYPE: DNA
186 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
189 Primer
190 <400> SEQUENCE: 9
191 cctatagctt tatgtccgca g 21
193 <210> SEQ ID NO: 10
194 <211> LENGTH: 27
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
199 Primer
200 <400> SEQUENCE: 10
201 ctttagcttc ccttaagtca ctctttg 27
203 <210> SEQ ID NO: 11
204 <211> LENGTH: 34

RAW SEQUENCE LISTING

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Input Set : N:\Crif3\RULE60\10090378.raw

Output Set: N:\CRF3\05012002\J090378.raw

205 <212> TYPE: PRT
206 <213> ORGANISM: Artificial Sequence
207 <220> FEATURE:
208 <223> OTHER INFORMATION: Description of Artificial Sequence:TPR Motifs
209 Consensus Sequence
W--> 210 <221> NAME/KEY: UNSURE
211 <222> LOCATION: (1)
212 <223> OTHER INFORMATION: Can be any large hydrophobic amino acid.
W--> 213 <221> UNSURE
214 <222> LOCATION: (2)..(3)
215 <223> OTHER INFORMATION: Can be any amino acid.
W--> 216 <221> UNSURE
217 <222> LOCATION: (4)
218 <223> OTHER INFORMATION: Can be any large hydrophobic amino acid.
W--> 219 <221> VARIANT
220 <222> LOCATION: (5)
221 <223> OTHER INFORMATION: Can be an Alanine as well.
W--> 222 <221> UNSURE
223 <222> LOCATION: (6)
224 <223> OTHER INFORMATION: Can be any amino acid.
W--> 225 <221> UNSURE
226 <222> LOCATION: (7)
227 <223> OTHER INFORMATION: Can be any large hydrophobic amino acid.
W--> 228 <221> VARIANT
229 <222> LOCATION: (8)
230 <223> OTHER INFORMATION: Can be a Phenylalanine as well.
W--> 231 <221> UNSURE
232 <222> LOCATION: (9)..(13)
233 <223> OTHER INFORMATION: Can be any amino acid.
W--> 234 <221> UNSURE
235 <222> LOCATION: (14)
236 <223> OTHER INFORMATION: Can be any large hydrophobic amino acid.
W--> 237 <221> UNSURE
238 <222> LOCATION: (15)..(16)
239 <223> OTHER INFORMATION: Can be any amino acid.
W--> 240 <221> UNSURE
241 <222> LOCATION: (18)
242 <223> OTHER INFORMATION: Can be any large hydrophobic amino acid.
W--> 243 <221> UNSURE
244 <222> LOCATION: (19)..(20)
245 <223> OTHER INFORMATION: Can be any amino acid.
W--> 246 <221> VARIANT
247 <222> LOCATION: (21)
248 <223> OTHER INFORMATION: Can be Tyrosine as well.
W--> 249 <221> UNSURE
250 <222> LOCATION: (22)..(23)
251 <223> OTHER INFORMATION: Can be any amino acid.
W--> 252 <221> UNSURE
253 <222> LOCATION: (25)

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1514,2066

Seq#:11; Xaa Pos. 1,2,3,4,6,7,9,10,11,12,13,14,15,16,18,19,20,22,23,25,26

Seq#:11; Xaa Pos. 27,28,30,31,32,33,34

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10090378.raw

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L:29 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1500
L:64 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2040
L:210 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:213 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:216 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:219 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:222 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:225 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:228 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:231 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:234 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:237 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:240 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:243 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:246 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:249 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:252 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:255 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:258 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:261 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:264 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:267 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:16
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:32